

IN THE CLAIMS

1. – 29. (cancelled)

30. (currently amended) A method of identifying a virus comprising:

contacting nucleic acid from said virus with at least one pair of primers which hybridize to flanking sequences of said nucleic acid, wherein said flanking sequences flank a variable nucleic acid sequence of said virus;

~~amplifying said nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family~~ said variable nucleic acid sequence to produce an amplification product;

~~measuring a~~ determining the base composition of said amplification product by mass spectrometry, wherein ~~the said~~ base composition identifies the number of A residues, C residues, T residues, G residues, U residues, analogues thereof and mass tag residues thereof in ~~the said~~ amplification product; and

comparing ~~the said~~ base composition of said amplification product ~~with known base compositions of amplification products of members of said viral family produced by using said pair of primers wherein a match of base composition of said amplification product with a known base composition of an amplification product of a member of said viral family indicates the identity of said virus.~~ to calculated or measured base compositions of analogous amplification products of one or more known viruses present in a database comprising 5 or more base compositions with the proviso that sequencing of said amplification product is not used to identify the virus.

31. (currently amended) The method of ~~Claim~~ claim 30, further comprising repeating said contacting, amplifying, ~~measuring~~ determining and comparing steps using one or more additional pairs of primers.

32. (currently amended) The method of ~~Claim~~ claim 30, wherein said virus is a biological warfare threat agent.
33. (currently amended) The method of ~~Claim~~ claim 30, wherein said virus is identified at the sub-species level.
- 34 – 49. (cancelled).
50. (currently amended) The method of claim 30₁ wherein said virus is a respiratory pathogen.
51. (currently amended) The method of claim 30₁ wherein said virus is a hepatitis C virus.
52. (currently amended) The method of claim 30₁ wherein said virus is an immunodeficiency virus.
53. (currently amended) The method of claim 30₁ wherein said virus is a member of a viral family selected from the group consisting of *Filoviridae*, *Flaviviridae*, *Arenaviridae*, *Bunyaviridae*, *Adenoviridae*, *Picornaviridae*, *Togaviridae*, and *Coronaviridae*.
54. (currently amended) The method of claim [[30]] 56, wherein said housekeeping gene is a polymerase, a virion component, a helicase, a protease, a methyltransferase, or an accessory protein.
55. (previously presented) The method of claim 54, wherein said polymerase is RNA-dependent RNA polymerase, DNA-dependent DNA polymerase or DNA-dependent RNA polymerase.
56. (new) The method of claim 30, wherein said nucleic acid is a housekeeping gene.

57. (new) The method of claim 30, wherein said amplifying step comprises the polymerase chain reaction.
58. (new) The method of claim 30, wherein the sequences to which the primers hybridize are separated by between about 60-100 nucleotides.
59. (new) The method of claim 30, wherein said virus is identified at the species level.
60. (new) The method of claim 30, wherein said pair of primers comprises at least one nucleotide analog.
61. (new) The method of claim 61, wherein said nucleotide analog is inosine, uridine, 2,6-diaminopurine, propyne C, or propyne T.
62. (new) The method of claim 30, wherein a molecular mass-modifying tag is incorporated into said amplification product to limit the number of possible base compositions consistent with the mass of said amplification product.